

## Plant Gene Register

A cDNA Encoding a Membrane Protein from Sugarcane<sup>1</sup>

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A sugarcane (*Saccharum* spp.) leaf cDNA library was screened with a 1.4-kb *EcoRV*-*BsmI* fragment of pTF414A (Glc transporter cDNA from *Arabidopsis thaliana*), which includes most of the coding region of the cDNA (Sauer et al., 1990). Plaque hybridizations were performed at low stringency with the random primed <sup>32</sup>P-labeled fragment of pTF414A followed by exposure of the nitrocellulose membranes to film for 48 h at -70°C. The cDNA of one of the positive clones was subcloned and sequencing revealed a cDNA of 1279 nucleotides. This cDNA (SMP1) contained an open reading frame encoding a polypeptide of 325 amino acids with a predicted molecular mass of 35.8 kD (Table I). The nucleotide sequence around the first Met of this open reading frame has 67% homology to the consensus translation initiation site of plants (Joshi, 1987).

Hydropathy analysis indicated that the SMP1 protein is a putative membrane protein. The grand average hydropathy value of the SMP1 protein was 0.38, significantly greater than the mean for soluble proteins (-0.4) (Kyte and Doolittle, 1982). This value is similar to values for membrane transport proteins for Glc (0.48) (Sauer et al., 1990) and Suc (0.57) (Riesmeier et al., 1992). In addition, SMP1 protein has a calculated isoelectric point (8.62) that is similar to that of the membrane transport proteins for Glc (9.49) and Suc (8.81). Furthermore, a hydropathy plot revealed that the deduced protein contains six putative membrane-spanning regions of 19 to 26 amino acids, with an average hydropathy index of >1.6 (Kyte and Doolittle, 1982).

The protein encoded by SMP1 does not share any significant overall homology with proteins in the GenBank, EMBL, and Swiss Protein data bases (Pearson and Lipman, 1988). The SMP1 sequence is 38% homologous at the nucleotide level to the fragment of the Glc transporter (pTF414A) used for screening the library, and shares 21% identity at the amino acid level with the Glc transporter.

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**Table I.** Characteristics of SMP1 cDNA from sugarcane

Organism:	<i>Saccharum</i> spp. hybrid cv H65-7052.
Location on Chromosome:	Unknown.
Function:	Encoding a 35.8-kD membrane protein.
Source:	cDNA library in $\lambda$ gt11 constructed with poly(A) <sup>+</sup> RNA of mature leaf tissue.
Techniques:	Heterologous screening of the cDNA library with a radiolabeled probe of pTF414A (cDNA clone for the Glc transporter from <i>A. thaliana</i> ).
Sequencing Strategy:	Deletion subcloning and double-stranded plasmid sequencing of both strands by the dideoxynucleotide chain termination method. Ambiguities were resolved using dITP.
Characteristics of Deduced Protein:	Open reading frame of 975 bp encoding a polypeptide of 325 amino acid residues of <i>M</i> , 35,867. Isoelectric point 8.62. The deduced protein contains six putative membrane spanning regions as determined by Kyte-Doolittle analysis with a window of 19 amino acids (Trp <sup>36</sup> -Met <sup>56</sup> , Leu <sup>117</sup> -Ile <sup>142</sup> , Ile <sup>153</sup> -Leu <sup>172</sup> , Thr <sup>201</sup> -Leu <sup>226</sup> , Phe <sup>232</sup> -Ala <sup>250</sup> , Ala <sup>273</sup> -Phe <sup>298</sup> ).
(G + C) Content:	Coding region 54.2%.
Antibodies:	None available.

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The GenBank accession number for the sequence reported in this article is L13655.

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